

Structure of HTPL and alignment of Patched motifs.

FIG. 1A
HTPL-L (954 a.a.)

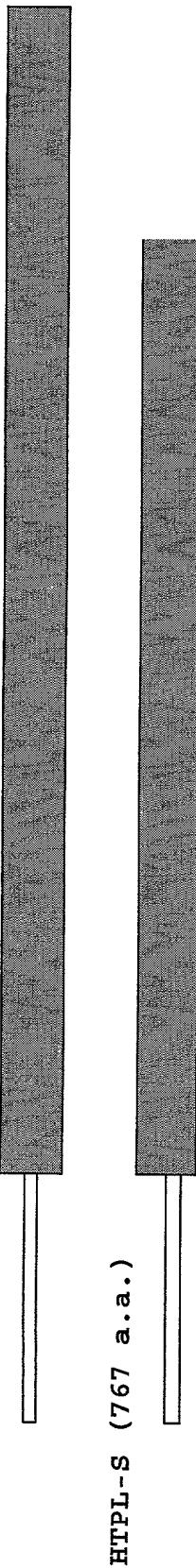


FIG. 1B
Patched motif

	10	20	30	40	50	60	70	80
consensus	...*...********
HTPL-L	1 VLSSKIRYTTPDDIIRSYTTERGSRSSEHEPL-VERKEFFPGDGYPI-SRFSIITAKARNS-NLDIRYLNEVVQYNDFTSTNV	78						
gi 1825729	162 deeedleehyTPGVSPAERRFVQGHFTTrADSYRFSAASRRSTEANFVSLIIVVSYSD-SLIDPATTAEVSKLDGAVQDLR	240						
gi 1707052	47 NPLSDAVYLFTPGLAQSKMERSMISHEKWPL-TDNYYIPGRAVTQSREIQVTZLARNDSNILDPKFANAVYQLDKYIQTRV	125						
gi 3892144	22 NVVYSUMLIFGPY--SYTERRILHDAWPL-VDGTFVAGRAVTQSREVQAVVARSGNILDDRVFSNELKLMESFIRNNI	97						
	49 LRVDDPSYVFTPSDARWRREISVNENWPL-DENKFLEPGKSFEAKRFVNILLRKDGGSIMRDNVILHEIEILNQWIMNNI	127						
	90	100	110	120	130	140	150	160
consensus	...*...********
HTPL-L	79 TIPVSG--ITLISFKDLCMRFCDCINCPVNQHYNGQILRSNLHNSRIDLTPTMTFFGTGKTYLGPNGFVGVKLDPN---PGN-	152						
gi 1825729	241 VAREKG--SQIQQQQVCARYRALCVPPNPILYYAQVNKTNLNS--SISFPAYNHGRHPLYLTGFFGGYILGGS---LGMg	313						
gi 1707052	126 RVLHNG--HYYSYKNLCLQYKNGGCPNSNKHV---HILSDLNHGGENITYPYFRFGSEGGYIGSSLGGVTVMKGeneTDI-	199						
gi 3892144	98 TVQFSN--RTWWSFADLCLAGpDGRCANNDHI---QLASRLHQHGINTYPTVRLSDKSAYIASALGGVKLAKGdngENTI-	171						
	128 SIPTDD1kFNFLTYQDLCLS-Y-DWVCGANEHIQ-MLLRNDVNQILDLHFPRGGTKDTPVYLGGLFGDVQFFFQn---GT-	200						

FIG. 1B

Patched motif (Continued)

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FIG. I

FIG. 1B
Patched motif (Continued)

	490	500	510	520	530	540	550	560
	* . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *							
consensus	417	--S-SKSHE--AEQ--AVVKFFFLNIYCPFLNPKVRCVCLLVLYVYLAIAYGCTNMKEGLDPAKL						
HTPL-L	572	--SVPDEHgTDIH--PMSLFFFRDYFGPFELTRSESKYFVVFIYLYIISIYGCFCFHQEGLDLRNL	475					
gi 1825729	469	--HSASHD--VKQP-LTSRFFGEWYAPVLMHPVVRGIAMWVFVYLLGASYGCSR.IKEGLEPVNL	632					
gi 1707052	451	--tsssstmtsgatSPASKH--LHHC-AATSSFFRNWYAPVLMQPWIRAIAGLWLYIYGISIYGC	528					
gi 3892144	515	ipaeafawkeqqspnss1SKSKD--REEkdrIVHFIGKLYGPFLNSVRIFSGLIFVYVYLAIAMYGC	522					
		NFREGLNPGNL	592					
	570	580	590	600	610	620	630	640
	* . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *							
consensus	476	FLKDDSLVEYLRLREKHVWPYGLQVTVFVNPPDLDLNENMDDEFENTPYAMGKRNSTKFWLRYENFLYSFISE	555					
HTPL-L	633	ASDDSYITTPYFNVEENYFSDYGPVRMVLYTCKVVDYWDKDVRQKLLENCTKLFEEKNVY-VDKNLTEFWL	709					
gi 1825729	529	LVEDSYAIPHYRLLEKFWKYGOQVQIVINNAPDLRNHTSRDRVHAMVLDEATSCHKHAIGMESVQFWLFEMER-	607					
gi 1707052	523	LYDDSYATPHYRVLeKHYWHYGAQLQIVVSNPPDLDVERINMDKMASTFANCKVAIGDDSVQFWLREMQ-	600					
gi 3892144	593	VINDHYIAKYFSDI-KHFWRIGAQQLHAVLNPPNLTTSENRMELLKVVSAFENTOYTGLGREGT	671					
		SELNAE	671					
	650	660	670	680	690	700	710	720
	* . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *							
consensus	556	LEDDEEEWWFYDILLEWFL-KSPGFISHWGDLVWDN-KTDYETTIVKKFRFTGGKDLSTWTDRTRLLKTWRGVADEYPDFN	633					
HTPL-L	710	QDPNEKNTFMNNIPDFLSNFPNFQH-----DI-NISSLNELLSSRGF-IOTTDYSSSAKKKILLFQLRRRA-EDCQIIP	779					
gi 1825729	608	VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGPMDDNGTMVKSFR.FILGMKDLVTTMDQTDATMSFREVAARWPEFNF	685					
gi 1707052	601	IQYDN-EKFYDHAAQYI-YSDMSQWPVVVDVWVG--RNNNNSERIIKTFRFMIGMRDISTTTKQTEATNTFREIASRFEQYN	676					
gi 3892144	672	VEDTERLWKTKLNSWLK-YTGGSTQWASNLIKIN-----KTDGSFQAFRFQIALKNFVEPNNDHKHAQLLRDIADHQ-P-FN	744					
	730	740	750	760	770	780	790	800
	* . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *							
consensus	634	VTIVEDED-----AFFLDQILSIGPTTIQSIIWTLICMAVVCFLFIPNPNTVFWITVSI	686					
HTPL-L	780	LMVYNQA-----FLYFDQYAAILEDTVRNVLVASAAMEFIVSLLLIPIYPLCSLWVTFAI	832					
gi 1825729	686	VTTFMPI-----WMFTDQYIIIIPNTVQNTIIALLVMIVIAVLFIFIOPQPMCSLWVALAC	738					
gi 1707052	677	VTTYMPL-----WLFDTQYALVVPNTMQDIIAVACMLVISALLIPQPVCSFWVAVTI	729					
gi 3892144	745	VVYHEVsfgnrkilndfisshsscyaqknipklaFPFADQYLLILPATIIONNVISLLCMAVVSFLVPSLPGFVIFVSI	824					

FIG. 1B

Patched motif (Continued)

	810	820	830	840	850	860	870	880
consensus	...*....********
HTPL-L	687 ASIDIGVFGFLSLWGVLDLDPISMIIIMSIGFSVDFSAHIAHYFYRSHGSETPDERILADEALGWPVVIQAAALSTILCVL	766						
gi	1825729 833 GSVIVGVTGFMAFWKVNLDISMINLVICIGFSFDSAHISYAFV-SSSQPSVNQKSVEALYLGYPVLSQSAISTIIGYC	911						
gi	1707052 739 ASIDFGVIGYMTLWGYNLDAISMIIIMSIGFSVDFSYSAHIAYGYVVSRED-TAACRVKEALSALGWPLSQGAMSTIIAVS	817						
gi	3892144 825 VSINIGVFGYMTLWGYNLDAVSMIIIMSIGFAVDLSAIIYAFVTSHG--DTKQRVIGALETLGWPIFIQGASSTIAGIS	902						
	890	900	910	920	930	940		
consensus******		
HTPL-L	767 PLLFVPSYMWFFFKTIFLFLVVFGLLHGLFLPLIPLSILFVT-----IRTSNAKKPSSI	821						
gi	1825729 912 VLAAKAYIFRTFFKIMFLVMIRGAAGHLIFIPVFLTFGRfi-----954							
gi	1707052 818 VIADIPAYMIVTFKTVVLSISLGLLHGLVFLPVLLS1FVRgccipssphGHPSAQKIERQIRI	882						
gi	3892144 903 IIXTVDAYIILVFFKTIWLTMLIGAIHGLEFFIPIFLSLFPV-----EFFRIPKSSET	954						

Structure of the HTPL gene (Chr. 10p12.1)

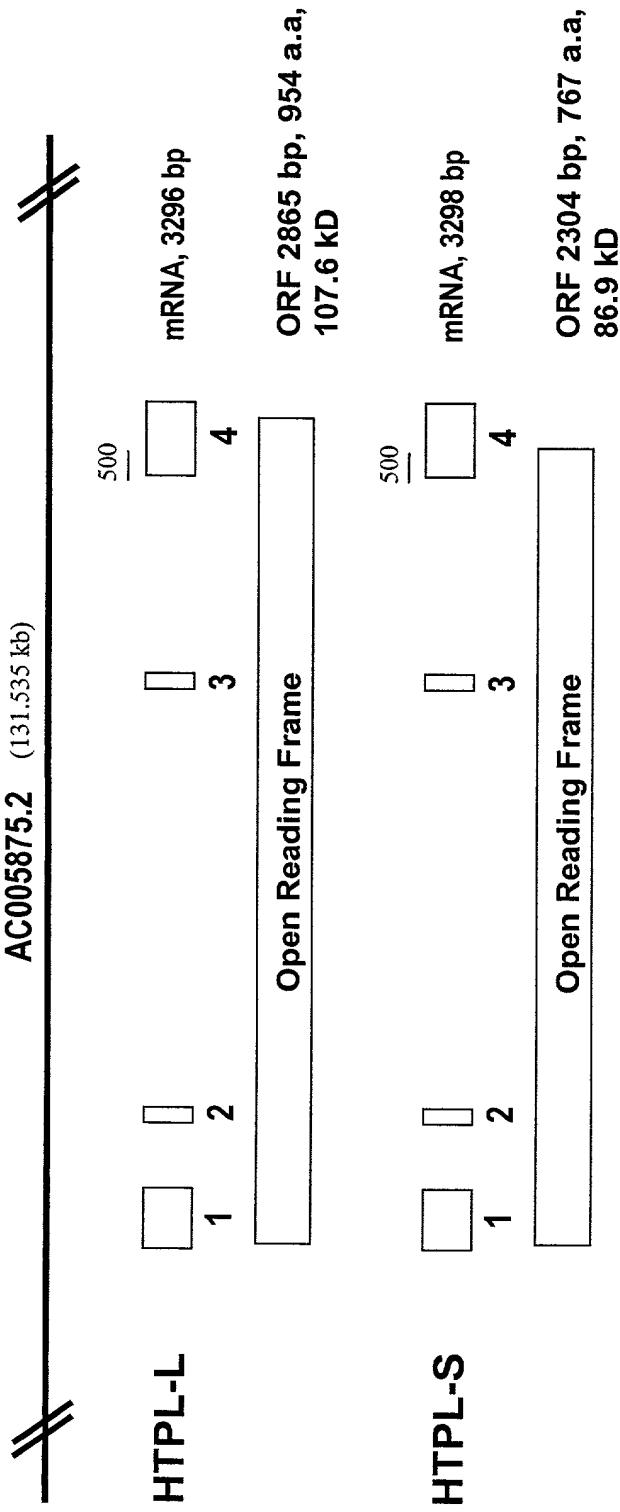


FIG. 2

HTPL-L

nt: SEQ ID NO: 1
aa: SEQ ID NO: 3

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTCACCTGCTGTTCC	52
CTGCGCTTCCTAACAGAGGAAGAATCA ATG CCG TGG GTG GAG CCC	95
K P R P G P E Q K P K L T AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC	19 134
K P D S A T G P Q W Y Q E AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA	32 173
S Q E S E S E G K Q P P P TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG	45 212
G P L A P P K S P E P S G GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA	58 251
P L A S E Q D A P L P E G CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG	71 290
D D A P P R P S M L D D A GAC GAT GCA CCC CCC CGG CCG TCG ATG CTG GAC GAT GCA	84 329
P R L P L E L D D A P L P CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG	97 368
E E E T P E P T A I C R H GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC	110 407
R H R C H T D C L E G L L CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG	123 446

FIG. 3

S	R	T	F	Q	W	L	G	W	Q	V	G	A		136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG		485
H	P	W	I	F	L	L	A	P	L	M	L	T		149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA		524
A	A	L	G	T	G	F	L	Y	L	P	K	D		162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC		563
E	E	E	D	L	E	E	H	Y	T	P	V	G		175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG		602
S	P	A	K	A	E	R	R	F	V	Q	G	H		188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT		641
F	T	T	N	D	S	Y	R	F	S	A	S	R		201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG		680
R	S	T	E	A	N	F	V	S	L	L	V	V		214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC		719
S	Y	S	D	S	L	L	D	P	A	T	F	A		227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA		758
E	V	S	K	L	D	G	A	V	Q	D	L	R		240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC		797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q		253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG		836
V	C	A	R	Y	R	A	L	C	V	P	P	N		266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC		875
P	I	L	Y	A	W	Q	V	N	K	T	L	N		279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC		914
L	S	S	I	S	F	P	A	Y	N	H	G	R		292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG		953
H	P	L	Y	L	T	G	F	F	G	G	Y	I		305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC		992

FIG. 3

L	G	G	S	L	G	M	G	Q	L	L	L	R		318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG		1031
A	K	A	M	R	L	L	Y	Y	L	K	T	E		331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG		1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T		344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC		1109
H	L	L	D	Q	F	T	N	I	K	N	I	L		357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG		1148
A	L	K	K	I	E	V	V	H	F	T	S	L		370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT		1187
S	R	Q	L	E	F	E	A	T	S	V	T	V		383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG		1226
I	P	V	F	H	L	A	Y	I	L	I	I	L		396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG		1265
F	A	V	T	S	C	F	R	F	D	C	I	R		409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA		1304
N	K	M	C	V	A	A	F	G	V	I	S	A		422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT		1343
F	L	A	V	V	S	G	F	G	L	L	L	H		435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC		1382
I	G	V	P	F	V	I	I	V	A	N	S	P		448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA		1421
F	L	I	L	G	V	G	V	D	D	M	F	I		461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC		1460
M	I	S	A	W	H	K	T	N	L	A	G	D		474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GGT	GAC		1499
I	R	E	R	M	S	N	V	Y	S	K	A	A		487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA		1538

FIG. 3

V	S	I	T	I	T	T	I	T	N	I	L	A		500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC		1577
L	Y	T	G	I	M	S	S	F	R	S	V	Q		513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCC	GTA	CAA		1616
C	F	C	I	Y	T	G	T	T	L	L	F	C		526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ACG	ACC	CTG	TTA	TTT	TGC		1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A		539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC		1694
L	D	G	K	R	E	V	V	C	L	C	W	L		552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG		1733
K	K	A	D	P	K	W	P	S	F	K	K	F		565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC		1772
C	C	F	P	F	G	S	V	P	D	E	H	G		578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA		1811
T	D	I	H	P	M	S	L	F	F	R	D	Y		591
ACT	GAT	ATC	CAT	CCA	ATG	AGT	TTG	TTT	TTT	AGA	GAC	TAT		1850
F	G	P	F	L	T	R	S	E	S	K	Y	F		604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT		1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I		617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA		1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R		630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA		1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F		643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT		2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R		656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG		2045
V	M	V	I	V	T	K	K	V	D	Y	W	D		669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT		2084

FIG. 3

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K	D	V	R	Q	K	L	E	N	C	T	K	I		682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT		2123
F	E	K	N	V	Y	V	D	K	N	L	T	E		695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG		2162
F	W	L	D	A	Y	V	Q	Y	L	K	G	N		708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC		2201
S	Q	D	P	N	E	K	N	T	F	M	N	N		721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT		2240
I	P	D	F	L	S	N	F	P	N	F	Q	H		734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT		2279
D	I	N	I	S	S	S	N	E	I	I	S	S		747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC		2318
R	G	F	I	Q	T	T	D	V	S	S	S	A		760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC		2357
K	K	K	I	L	L	F	Q	L	R	R	I	A		773
AAA	AAG	AAA	ATA	TTG	TTA	TTC	CAA	TTA	CGA	CGC	ATA	GCT		2396
E	D	C	Q	I	P	L	M	V	Y	N	Q	A		786
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA		2435
F	I	Y	F	D	Q	Y	A	A	I	L	E	D		799
TTT	ATA	TAT	TTT	GAT	CAG	TAT	GCT	GCA	ATA	TTA	GAA	GAC		2474
T	V	R	N	V	L	V	A	S	A	A	M	F		812
ACT	GTT	AGA	AAT	GTA	TTG	GTT	GCA	TCA	GCA	GCT	ATG	TTC		2513
I	V	S	L	L	L	I	P	Y	P	L	C	S		825
ATT	GTT	TCC	TTA	TTG	TTA	ATC	CCT	TAT	CCA	TTG	TGT	TCC		2552
L	W	V	T	F	A	I	G	S	V	I	V	G		838
TTG	TGG	GTG	ACT	TTT	GCT	ATC	GGT	TCT	GTG	ATT	GTA	GGG		2591
V	T	G	F	M	A	F	W	K	V	N	L	D		851
GTA	ACG	GGT	TTC	ATG	GCA	TTC	TGG	AAA	GTC	AAT	CTT	GAT		2630

FIG. 3

S	I	S	M	I	N	L	V	I	C	T	G	F	864
TCC	ATA	TCC	ATG	ATT	AAT	CTT	GTC	ATT	TGT	ACA	GGG	TTT	2669
S	F	D	F	S	A	H	I	S	Y	A	F	V	877
TCT	TTC	GAT	TTT	TCT	GCA	CAC	ATT	TCC	TAT	GCA	TTT	GTT	2708
S	S	S	Q	P	S	V	N	Q	K	S	V	E	890
TCT	AGT	TCT	CAA	CCC	TCA	GTA	AAC	CAA	AAA	TCA	GTT	GAG	2747
A	L	Y	L	L	G	Y	P	V	L	Q	S	A	903
GCA	TTG	TAT	CTT	CTA	GGC	TAC	CCA	GTG	TTA	CAA	AGT	GCA	2786
I	S	T	I	I	G	V	C	V	L	A	A	A	916
ATT	TCA	ACA	ATA	ATA	GGG	GTG	TGT	GTT	TTA	GCT	GCA	GCG	2825
K	A	Y	I	F	R	T	F	F	K	I	M	F	929
AAA	GCA	TAC	ATC	TTC	AGA	ACA	TTT	TTT	AAG	ATT	ATG	TTT	2864
L	V	M	I	F	G	A	A	H	G	L	I	F	942
CTT	GTT	ATG	ATA	TTT	GGG	GCA	GCT	CAT	GGC	CTA	ATT	TTT	2903
I	P	V	F	L	T	F	F	G	R	F	I	*	955
ATT	CCA	GTA	TTC	TTA	ACC	TTT	TTT	GGA	AGG	TTT	ATT	TGA	2942
ATATCCACTAACAAAGTCAAAGACCAATTCTAGAATTCCCTGATTGCCCTATT													2994
CAATCTGATTTTTAAATGCACTATTAAGAATAGTCAACAAACTACTGGGA													3046
GGCCAAAGTGGGTGGATCACCTGAGGTCAAGAATTGAGACCAGCCTGGCCA													3098
ACATGGTGAAACCTCGACACTACTGAAAATACAAAAATTATCCAGGCATGGT													3150
GGCGTGCACCTATAATCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCT													3202
TGAACCTGGGAGATGGAGGTTGCAGTGAGCTGGAGTGCACCAGGCACTCCAG													3254
CCTGGGTGACAAGAATGAGACTCCGTCTCAGAAAAAAAAAAA													3296

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HTPL-S

nt: SEQ ID NO: 4
aa: SEQ ID NO: 6

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTCACCTGCTGTTCCCTC	52
CTGCGCTTCCTAACAGAGGAAGAATCA ATG CCG TGG GTG GAG CCC	95
K P R P G P E Q K P K L T	19
AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC	134
K P D S A T G P Q W Y Q E	32
AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA	173
S Q E S E S E G K Q P P P	45
TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG	212
G P L A P P K S P E P S G	58
GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA	251
P L A S E Q D A P L P E G	71
CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG	290
D D A P P R P S M L D D A	84
GAC GAT GCA CCC CCC CGG CCG TCG ATG CTG GAC GAT GCA	329
P R L P L E L D D A P L P	97
CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG	368
E E E T P E P T A I C R H	110
GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC	407
R H R C H T D C L E G L L	123
CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG	446
S R T F Q W L G W Q V G A	136
TCC CGC ACC TTC CAG TGG CTG GGG TGG CAG GTG GGC GCG	485

FIG. 4

H	P	W	I	F	L	L	A	P	L	M	L	T		149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA		524
A	A	L	G	T	G	F	L	Y	L	P	K	D		162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC		563
E	E	E	D	L	E	E	H	Y	T	P	V	G		175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG		602
S	P	A	K	A	E	R	R	F	V	Q	G	H		188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT		641
F	T	T	N	D	S	Y	R	F	S	A	S	R		201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG		680
R	S	T	E	A	N	F	V	S	L	L	V	V		214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC		719
S	Y	S	D	S	L	L	D	P	A	T	F	A		227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA		758
E	V	S	K	L	D	G	A	V	Q	D	L	R		240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC		797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q		253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG		836
V	C	A	R	Y	R	A	L	C	V	P	P	N		266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC		875
P	I	L	Y	A	W	Q	V	N	K	T	L	N		279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC		914
L	S	S	I	S	F	P	A	Y	N	H	G	R		292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG		953
H	P	L	Y	L	T	G	F	F	G	G	Y	I		305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC		992
L	G	G	S	L	G	M	G	Q	L	L	L	R		318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG		1031

FIG. 4

A	K	A	M	R	L	L	Y	Y	L	K	T	E		331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG		1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T		344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC		1109
H	L	L	D	Q	F	T	N	I	K	N	I	L		357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG		1148
A	L	K	K	I	E	V	V	H	F	T	S	L		370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT		1187
S	R	Q	L	E	F	E	A	T	S	V	T	V		383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG		1226
I	P	V	F	H	L	A	Y	I	L	I	I	L		396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG		1265
F	A	V	T	S	C	F	R	F	D	C	I	R		409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA		1304
N	K	M	C	V	A	A	F	G	V	I	S	A		422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT		1343
F	L	A	V	V	S	G	F	G	L	L	L	H		435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC		1382
I	G	V	P	F	V	I	I	V	A	N	S	P		448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA		1421
F	L	I	L	G	V	G	V	D	D	M	F	I		461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC		1460
M	I	S	A	W	H	K	T	N	L	A	D	D		474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GAT	GAC		1499
I	R	E	R	M	S	N	V	Y	S	K	A	A		487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA		1538
V	S	I	T	I	T	T	I	T	N	I	L	A		500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC		1577

FIG. 4

L	Y	T	G	I	M	S	S	F	R	S	V	Q		513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCT	GTA	CAA		1616
C	F	C	I	Y	T	G	M	T	L	L	F	C		526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ATG	ACC	CTG	TTA	TTT	TGC		1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A		539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC		1694
L	D	G	K	R	E	V	V	C	L	C	W	L		552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG		1733
K	K	A	D	P	K	W	P	S	F	K	K	F		565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC		1772
C	C	F	P	F	G	S	V	P	D	E	H	G		578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA		1811
T	D	I	H	P	I	S	L	F	F	R	D	Y		591
ACT	GAT	ATC	CAT	CCA	ATA	AGT	TTG	TTT	TTT	AGA	GAC	TAT		1850
F	G	P	F	L	T	R	S	E	S	K	Y	F		604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT		1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I		617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA		1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R		630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA		1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F		643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT		2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R		656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG		2045
V	M	V	I	V	T	K	K	V	D	Y	W	D		669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT		2084
K	D	V	R	Q	K	L	E	N	C	T	K	I		682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT		2123
F	E	K	N	V	Y	V	D	K	N	L	T	E		695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG		2162

FIG. 4

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F	W	L	D	A	Y	V	Q	Y	L	K	G	N		708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC		2201
S	Q	D	P	N	E	K	N	T	F	M	N	N		721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT		2240
I	P	D	F	L	S	N	F	P	N	F	Q	H		734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT		2279
D	I	N	I	S	S	S	N	E	I	I	S	S		747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC		2318
R	G	F	I	Q	T	T	D	V	S	S	S	A		760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC		2357
K	K	K	I	L	L	F	*							768
AAA	AAG	AAA	ATA	TTG	TTA	TTC	TAA	TTACGACGCATAGCTGAAG						2400
ACTGTCAAATTCCCTAATGGTGTATAACCAGGCATTATATATTTGATCA														2452
GTATGCTGCAATATTAGAACACTGTTAGAAATGTATTGGTGCATCAGCA														2504
GCTATGTCATTGTTCTTATTGTAATCCCTATCCATTGTTCTGT														2556
GGGTGACTTTGCTATTGGCTGTGATTGTAGGGTAACGGGTTCATGGC														2608
ATTCTGGAAAGTCAATCTGATTCCATATCCATGATTAATCTGTCATTGT														2660
ATAGGGTTTCTTCGATTTCTGTACACATTCCTATGCATTGTTCTA														2712
GTTCTCAACCCTCAGTAAACAAAAATCAGTTGAGGCATTGTATCTTAGG														2764
CTACCCAGTGTACAAAGTCAATTCAACAATAATAGGGTGTGTTTA														2816
GCTGCAGCGAAAGCATACTTCAGAACATTTTAAGATTATGTTCTTG														2868
TTATGATATTGGGGCAGCTCATGCCCTAATTTTATTCCAGTATTCTAAC														2920
CTTTTTGGAAGGTTATTGAATATCCACTAACAAAGTCAAAGACCAATTCT														2972
AGAATTCCCTGATTGCCCTATTCCAATCTGATTTTAAATGCACTATTAAG														3024
AATAGTCAACAAACTACTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAA														3076

FIG. 4

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GAATTCGAGACCAGCCTGGCCAACATGGTAAACCTCGACACTACTGAAAAT 3128
ACAAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG 3180
AGGCTGAGGCAGGAGAACGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC 3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA 3284
GAAAAAAAAAAAAA 3298

FIG. 4

HTPL tissue distribution by RT-PCR

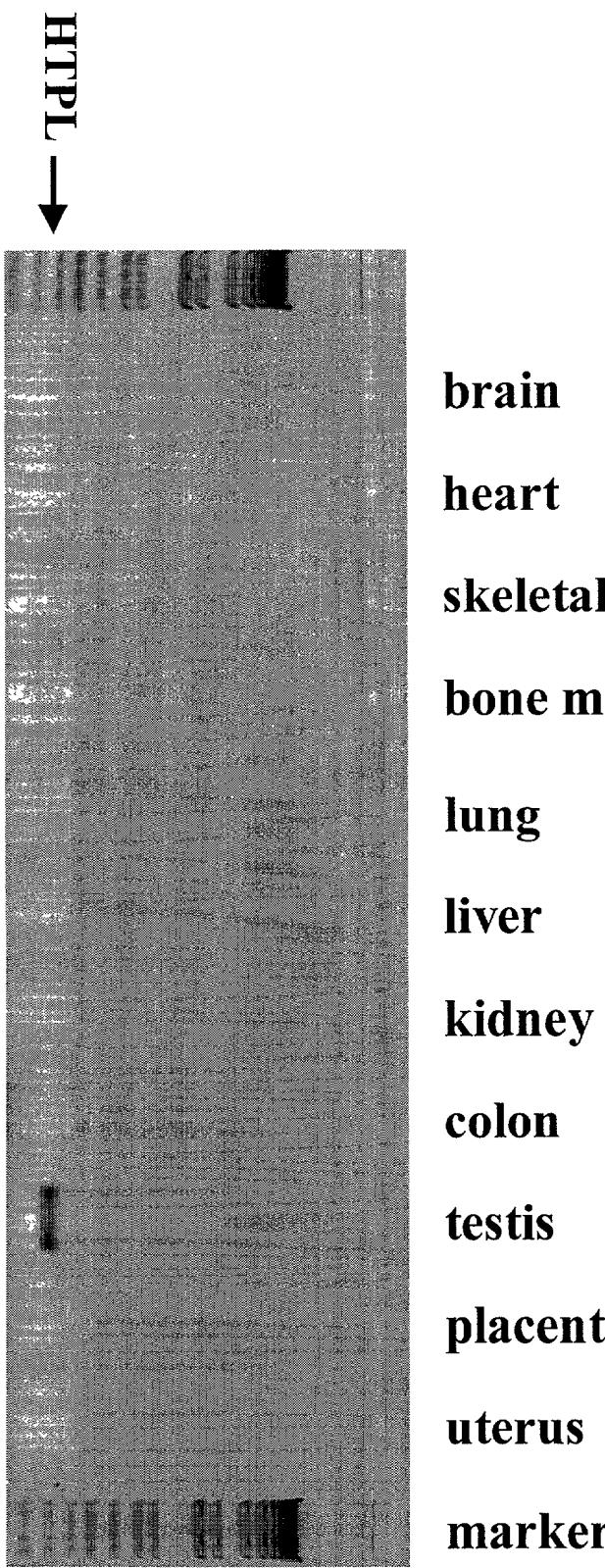


FIG. 5